



SEQUENCE LISTING

<110> Moore, Rachael
Dudley, Adam Jeston

<120> METHODS FOR THE DETECTION OF POLYMORPHISMS IN THE HUMAN OATPF GENE

<130> 06275-422US1

<150> PCT/GB03/02487

<151> 2003-06-10

<150> GB 0213580.4

<151> 2002-06-13

<150> US 60/388,692

<151> 2002-06-14

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR forward
primer OATPF-1F

<400> 1

actgtaaaac gacggccagt aatgaggctt aaactgggca

40

<210> 2

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR reverse
primer OATPF-1R

<400> 2

accaggaaac agctatgacc ggtagagatt gcttgcaccg

40

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Validation
primer

<400> 3
 tggacacttc atccaaagaa 20

<210> 4
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR forward
 primer OATPF-2F

<400> 4
 actgtaaaac gacggccagt ctatgagcca gatcttctgg c 41

<210> 5
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR reverse
 primer OATPF-2R

<400> 5
 accaggaaac agctatgacc cagaagcttt gaaagatttt ccc 43

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Validation
 primer

<400> 6
 tattctcctt cctccaattc 20

<210> 7
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR forward
 primer OATPF-3F

<400> 7
 actgtaaaac gacggccagt tgggcaccta attgctacct 40

<210> 8
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR reverse
 primer OATPF-3R

<400> 8
 accaggaaac agctatgacc tgaggaaca tacccttggt 40

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Validation
 primer

<400> 9
 atcagtgtgt gtggagctgc 20

<210> 10
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR forward
 primer OATPF-4F

<400> 10
 actgtaaaac gacggccagt gctgttctag gcaaacaggg 40

<210> 11
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR reverse
 primer OATPF-4R

<400> 11
 ccagtagttg ggttgt 16

<210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Validation
primer

<400> 12

cttcttcttag acatatatat

20

<210> 13

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR forward
primer OATPF-5F

<400> 13

actgtaaaac gacggccagt cttcagctct ttctgtgccc

40

<210> 14

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR reverse
primer OATPF-5R

<400> 14

accaggaac agctatgacc ttccatcaaa ctaatgaggg g

41

<210> 15

<211> 54

<212> DNA

<213> Homo sapiens

<400> 15

atcttttactt taaaaaactaa ctttgacaga tcagagtcaa ggaatgtgtt tata

54

<210> 16

<211> 3077

<212> DNA

<213> Homo sapiens

<400> 16

cattgaaagg aaatggctat ctttgatctc ttcctccaga tcagagtcaa ggaatgtgtt 60
tataatggac acttcatcca aagaaaatat ccagttgttc tgcaaaactt cagtgcacc 120
tggtggaagg cttcttttta aaacagaata tccctcctca gaagaaaagc aaccatgctg 180
tggtgaacta aaggtgttct tgtgtgcctt gtcttttggt tactttgcca aagcattggc 240
agaaggctat ctgaagagca ccatcactca gatagagaga aggtttgata tcccttcttc 300
actggtggga gttattgatg gtagttttga aattgggaat ctcttagtta taacatttgt 360
tagctacttt ggagccaaac ttcacaggcc aaaaataatt ggagcagggt gtgtaatcat 420
gggagttgga acactgctca ttgcaatgcc tcagttcttc atggagcagt acaaatatga 480

```

gagatattct ccttctcca attccactct cagcatctct ccgtgtctcc tagagtcaag 540
cagtcaatta ccagtttcag ttatggaaaa atcaaaatcc aaaataagta acgaatgtga 600
agtggaact agctcttcca tgtggattta tgttttcttg ggcaatcttc ttcgtggaat 660
aggagaaact ccattcagc ctttgggcat tgcctacctg gatgattttg ccagtgaaga 720
caatgcagct ttctatattg ggtgtgtgca gacggttgca attataggac caatctttgg 780
tttctgttta ggctcattat gtgccaaact atatgttgac attggctttg taaacctaga 840
tcacataacc attaccccaa aagatcccca gtgggtagga gcctgggtggc ttggctatct 900
aatagcagga atcataagtc ttcttgacgc tgtgcctttc tggatatttac caaagagttt 960
accaagatcc caaagtagag aggattctaa ttcttctctc gagaaatcca agttttattat 1020
agatgatcac acagactacc aaacacccca gggagaaaat gcaaaaataa tggaaatggc 1080
aagagatttt cttccatcac tgaagaatct ttttggaaac ccagtatact tcctatattt 1140
atgtacaagc actgttcagt tcaattctct gttcggcatg gtgacgtaca aaccaaaagta 1200
cattgagcag cagtatggac agtcaccttc cagggccaac tttgtgatcg ggctcatcaa 1260
cattccagca gtggcccttg gaattttctc tggggggata gttatgaaaa aattcagaat 1320
cagtgtgtgt ggagctgcaa aactctactt gggatcatct gtctttgggtt acctcctatt 1380
tctttccctg tttgcactgg gctgtgaaaa ttctgatgtg gcaggactaa ctgtctccta 1440
ccaaggaacc aaacctgtct cttatcatga acgagctctc ttttcagatt gcaactcaag 1500
atgcaaatgt tcagagacaa aatgggaacc catgtgcggt gaaaatggaa tcacatatgt 1560
atcagcttgt cttgctgggt gtcaaacctc caacaggagt ggaaaaaata ttatatttta 1620
caactgcact tgtgtgggaa ttgcagcttc taaatccgga aattcctcag gcatagtggg 1680
aagatgtcag aaagacaatg gatgtcccca aatgtttctg tatttccttg taatttcagt 1740
catcacatcc tatactttat ccctagggtg catacctgga tacatattac ttctgagggtg 1800
cattaagcca cagcttaagt cttttgcctt gggatatctac acattagcaa taagagtctt 1860
tgcaggaatc ccagctccag tgtatttttg agttttgatt gatacttcat gcctcaaagt 1920
gggattttaa agatgtggaa gtagaggatc atgcagatta tatgattcaa atgtcttcag 1980
acatatatat ctgggactaa ctgtgatact gggcacagtg tcaattctcc taagcattgc 2040
agtacttttc attttaaaga aaaattatgt ttcaaaacac agaagtttta taaccaagag 2100
agaaagaaca atggtgtcta caagattcca aaaggaaaat tacactacaa gtgatcatct 2160
gtacaaccc aactactggc caggcaagga aactcaactt tagaaacatg atgactggaa 2220
gtcatgtctt ctaattgggt gacattttgc aaacaaataa attgtaatca aaagagctct 2280
aaatttgtaa tttctttctc ctttcaaaaa atgtctactt tgttttggtc ctaggcatta 2340
ggtaataata ctgataatat actgaaacat ataatggaag atgcagatga taaaactaat 2400
tttgaacttt ttaatttata taaattatgt tatactactt acttatttca ctttattttg 2460
ctttgtgctc attgatatat attagctgta ctctagaag aacaattgtc tctattgtca 2520
cacatgggta tattttaaagt aatttctgaa ctgtgtaatg tgtctagagt aagcaaatc 2580
tgctaacaat taactcatac cttgggttcc ttcaagtatt actcctatag tattttctcc 2640
catagctgtc ttcatctgtg tattttaata atgatcttag gatggagcag aacatggaga 2700
ggaagatttc attttaagct cctccttttc tttgaaatac aataatttat atagaaatgt 2760
gtagcagcaa attatattgg ggattagaat tttgaattaa tagctctcct actattaatt 2820
tacatgtgct ttttgtgtgg cgctataagt gactatgggt gttaaagtaat aaaattgatg 2880
ttaacatgcc caattattgt tcttttatga attcaatgaa tttaaaacta ttgttaaata 2940
taatactgcc ccactttaat atatgtaagc aacttcctac ttatacacga cgtgttccta 3000
aaacatgttt gaaaggtgaa tttctgaaag tctacaataa atgtaggtgt tacaacagga 3060
aaaaaaaaa aaaaaaa 3077

```

<210> 17

<211> 712

<212> PRT

<213> Homo sapiens

<400> 17

```

Met Asp Thr Ser Ser Lys Glu Asn Ile Gln Leu Phe Cys Lys Thr Ser
  1                      5                      10                      15

```

```

Val Gln Pro Val Gly Arg Pro Ser Phe Lys Thr Glu Tyr Pro Ser Ser
      20                      25                      30

```

Glu Glu Lys Gln Pro Cys Cys Gly Glu Leu Lys Val Phe Leu Cys Ala
 35 40 45
 Leu Ser Phe Val Tyr Phe Ala Lys Ala Leu Ala Glu Gly Tyr Leu Lys
 50 55 60
 Ser Thr Ile Thr Gln Ile Glu Arg Arg Phe Asp Ile Pro Ser Ser Leu
 65 70 75 80
 Val Gly Val Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val Ile
 85 90 95
 Thr Phe Val Ser Tyr Phe Gly Ala Lys Leu His Arg Pro Lys Ile Ile
 100 105 110
 Gly Ala Gly Cys Val Ile Met Gly Val Gly Thr Leu Leu Ile Ala Met
 115 120 125
 Pro Gln Phe Phe Met Glu Gln Tyr Lys Tyr Glu Arg Tyr Ser Pro Ser
 130 135 140
 Ser Asn Ser Thr Leu Ser Ile Ser Pro Cys Leu Leu Glu Ser Ser Ser
 145 150 155 160
 Gln Leu Pro Val Ser Val Met Glu Lys Ser Lys Ser Lys Ile Ser Asn
 165 170 175
 Glu Cys Glu Val Asp Thr Ser Ser Ser Met Trp Ile Tyr Val Phe Leu
 180 185 190
 Gly Asn Leu Leu Arg Gly Ile Gly Glu Thr Pro Ile Gln Pro Leu Gly
 195 200 205
 Ile Ala Tyr Leu Asp Asp Phe Ala Ser Glu Asp Asn Ala Ala Phe Tyr
 210 215 220
 Ile Gly Cys Val Gln Thr Val Ala Ile Ile Gly Pro Ile Phe Gly Phe
 225 230 235 240
 Leu Leu Gly Ser Leu Cys Ala Lys Leu Tyr Val Asp Ile Gly Phe Val
 245 250 255
 Asn Leu Asp His Ile Thr Ile Thr Pro Lys Asp Pro Gln Trp Val Gly
 260 265 270
 Ala Trp Trp Leu Gly Tyr Leu Ile Ala Gly Ile Ile Ser Leu Leu Ala
 275 280 285
 Ala Val Pro Phe Trp Tyr Leu Pro Lys Ser Leu Pro Arg Ser Gln Ser
 290 295 300
 Arg Glu Asp Ser Asn Ser Ser Ser Glu Lys Ser Lys Phe Ile Ile Asp
 305 310 315 320
 Asp His Thr Asp Tyr Gln Thr Pro Gln Gly Glu Asn Ala Lys Ile Met
 325 330 335

Glu Met Ala Arg Asp Phe Leu Pro Ser Leu Lys Asn Leu Phe Gly Asn
 340 345 350
 Pro Val Tyr Phe Leu Tyr Leu Cys Thr Ser Thr Val Gln Phe Asn Ser
 355 360 365
 Leu Phe Gly Met Val Thr Tyr Lys Pro Lys Tyr Ile Glu Gln Gln Tyr
 370 375 380
 Gly Gln Ser Ser Ser Arg Ala Asn Phe Val Ile Gly Leu Ile Asn Ile
 385 390 395 400
 Pro Ala Val Ala Leu Gly Ile Phe Ser Gly Gly Ile Val Met Lys Lys
 405 410 415
 Phe Arg Ile Ser Val Cys Gly Ala Ala Lys Leu Tyr Leu Gly Ser Ser
 420 425 430
 Val Phe Gly Tyr Leu Leu Phe Leu Ser Leu Phe Ala Leu Gly Cys Glu
 435 440 445
 Asn Ser Asp Val Ala Gly Leu Thr Val Ser Tyr Gln Gly Thr Lys Pro
 450 455 460
 Val Ser Tyr His Glu Arg Ala Leu Phe Ser Asp Cys Asn Ser Arg Cys
 465 470 475 480
 Lys Cys Ser Glu Thr Lys Trp Glu Pro Met Cys Gly Glu Asn Gly Ile
 485 490 495
 Thr Tyr Val Ser Ala Cys Leu Ala Gly Cys Gln Thr Ser Asn Arg Ser
 500 505 510
 Gly Lys Asn Ile Ile Phe Tyr Asn Cys Thr Cys Val Gly Ile Ala Ala
 515 520 525
 Ser Lys Ser Gly Asn Ser Ser Gly Ile Val Gly Arg Cys Gln Lys Asp
 530 535 540
 Asn Gly Cys Pro Gln Met Phe Leu Tyr Phe Leu Val Ile Ser Val Ile
 545 550 555 560
 Thr Ser Tyr Thr Leu Ser Leu Gly Gly Ile Pro Gly Tyr Ile Leu Leu
 565 570 575
 Leu Arg Cys Ile Lys Pro Gln Leu Lys Ser Phe Ala Leu Gly Ile Tyr
 580 585 590
 Thr Leu Ala Ile Arg Val Leu Ala Gly Ile Pro Ala Pro Val Tyr Phe
 595 600 605
 Gly Val Leu Ile Asp Thr Ser Cys Leu Lys Trp Gly Phe Lys Arg Cys
 610 615 620
 Gly Ser Arg Gly Ser Cys Arg Leu Tyr Asp Ser Asn Val Phe Arg His
 625 630 635 640

Ile Tyr Leu Gly Leu Thr Val Ile Leu Gly Thr Val Ser Ile Leu Leu
 645 650 655

Ser Ile Ala Val Leu Phe Ile Leu Lys Lys Asn Tyr Val Ser Lys His
 660 665 670

Arg Ser Phe Ile Thr Lys Arg Glu Arg Thr Met Val Ser Thr Arg Phe
 675 680 685

Gln Lys Glu Asn Tyr Thr Thr Ser Asp His Leu Leu Gln Pro Asn Tyr
 690 695 700

Trp Pro Gly Lys Glu Thr Gln Leu
 705 710